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SEQUENCE LISTING

70510 (1) GENERAL INFORMATION:

- (i) APPLICANT: Pelus, Louis M
Bhatnagar, Pradip K
King, Andrew G
Balcarek, Joanna M
- (ii) TITLE OF INVENTION: Methods of Enhancing Bioactivity of Chemokines
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SmithKline Beecham Corporation - Corporate Patents
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-2799
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hall, Linda E.
(B) REGISTRATION NUMBER: 31,763
(C) REFERENCE DOCKET NUMBER: SBC P50161
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Ile | Ala | Asn | Glu | Leu | Arg | Cys | Gln | Cys | Leu | Gln | Thr | Met | Ala |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

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Gly Ile His Leu Lys Asn Ile Gln Ser Leu Lys Val Leu Pro Ser Gly
 20 25 30
 Pro His Cys Thr Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Arg
 35 40 45
 Glu Ala Cys Leu Asp Pro Glu Ala Pro Leu Val Gln Lys Ile Val Gln
 50 55 60
 Lys Met Leu Lys Gly Val Pro Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
 1 5 10 15
 Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser Pro Gly
 20 25 30
 Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Arg
 35 40 45
 Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile Ile Glu
 50 55 60
 Lys Met Leu Asn Ser Asp Lys Ser Asn
 65 70

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
 1 5 10 15
 Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser Pro Gly
 20 25 30
 Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Gln
 35 40 45

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Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile Ile Glu
 50 55 60

Lys Met Leu Lys Asn Gly Lys Ser Asn
 65 70

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ser Val Val Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
 1 5 10 15

Gly Ile His Leu Lys Asn Ile Gln Ser Val Asn Val Arg Ser Pro Gly
 20 25 30

Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Lys
 35 40 45

Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln Lys Ile Ile Glu
 50 55 60

Lys Ile Leu Asn Lys Gly Ser Thr Asn
 65 70

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image of peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminosuberic acid."

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(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Glu Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)2 which bonds to mirror image of peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminoadipic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Glu Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Glu bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image of peptide."

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(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminosuberic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Xaa Glu Glu Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds (CH2)4 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminosuberic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Asp Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..3
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is picolinic acid (Pic)."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminosuberic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Xaa Glu Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..3
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is L-pipecolinic acid (L-Ppc)."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminosuberic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Xaa Glu Asp Xaa Lys
1 5

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminosuberic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Xaa Ser Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)2 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminoadipic acid."

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(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa Ser Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, position 5
Xaa bonds to CO, both NH & CO bond to CH which
bonds to (CH2)2 which bonds to identical peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminoadipic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 5 is Lys-NH2."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Ser Asp Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..3
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is picolinic acid (Pic)."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)2 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminoadipic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Ser Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..3
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is picolinic acid (Pic)."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, position 5 Xaa bonds to CO, both NH & CO bond to CH which bonds to (CH2)2 which bonds to identical peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 5 is Lys-NH2."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminoadipic acid."

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Xaa Ser Asp Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Tyr bonds to CO, both NH and CO bond to CH which bonds to (CH2)2 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminoadipic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Xaa Glu Asp Xaa Tyr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..3
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is picolinic acid (Pic)."

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(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)2 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminoadipic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Xaa Glu Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, position 5 Xaa bonds to CO, both NH & CO bond to CH which bonds to (CH2)4 which bonds to identical peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminosuberic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 5 is Lys-NH2."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Xaa Glu Asp Xaa Xaa
1 5

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(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 1..3
(D) OTHER INFORMATION: /note= "Xaa in position 1 is
picolinic acid (Pic)."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 3..5
(D) OTHER INFORMATION: /note= "Asp bonds to NH, position 5
Xaa bonds to CO, both NH & CO bond to CH which
bonds to (CH2)2 which bonds to identical peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 3..5
(D) OTHER INFORMATION: /note= "Xaa in position 5 is
Lys-NH2."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 3..5
(D) OTHER INFORMATION: /note= "Xaa in position 4 is
diaminoadipic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Xaa Glu Asp Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 3..5
(D) OTHER INFORMATION: /note= "Asp is bound to NH and Lys
is bound to CO, NH and CO are bound to (CH2)3
which is bound to a mirror image of this peptide."

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(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminopimelic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Xaa Glu Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is Lanthionine [SCH₂CH(NH₂)COOH] which acts as a bridge linking a mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Xaa Glu Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminopimelic acid."

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(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp is bound to NH and position 5 Xaa is bound to CO, NH & CO are bound to (CH2)3 which is bound to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 5 is Arg-CONH2"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Xaa Glu Asp Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa is diaminosuberic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Glu Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4..6
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which is bond to (CH2)4 which bonds to a mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4..6
- (D) OTHER INFORMATION: /note= "Xaa in position 5 is diaminosuberic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Xaa Tyr Glu Asp Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4..6
- (D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which is bond to (CH2)4 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4..6
- (D) OTHER INFORMATION: /note= "Xaa in position 5 is diaminosuberic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Xaa Glu Tyr Asp Xaa Lys
1 5

605

65

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4..6
- (D) OTHER INFORMATION: /note= "Tyr bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4..6
- (D) OTHER INFORMATION: /note= "Xaa in position 5 is diaminosuberic acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Xaa Glu Asp Tyr Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..5
- (D) OTHER INFORMATION: /note= "Xaa in position 4 is bis BOC-S,S'-1,3-propanediylcysteine (Prc) which acts as a bridge linking a mirror image peptide."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..2
- (D) OTHER INFORMATION: /note= "Xaa in position 1 is pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Xaa Glu Asp Xaa Lys
1 5

66

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..3
(D) OTHER INFORMATION: /note= "Xaa in position 1 is the d-form of pyroglutamic acid."
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3..5
(D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image peptide."
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3..5
(D) OTHER INFORMATION: /note= "Xaa in position 4 is diaminosuberic acid."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
- | | | | | |
|-----|-----|-----|-----|-----|
| Xaa | Glu | Asp | Xaa | Lys |
| 1 | | | | 5 |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..3
(D) OTHER INFORMATION: /note= "Glu is in the d-form."
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3..5
(D) OTHER INFORMATION: /note= "Asp bonds to NH, Lys bonds to CO, both NH and CO bond to CH which bonds to (CH2)4 which bonds to mirror image peptide."

(A) NAME/KEY: Modified-site

(B) LOCATION: 3..5

(D) OTHER INFORMATION: /note= "Xaa in position 4 is
diaminosuberic acid."

(A) NAME/KEY: Modified-site

(B) LOCATION: 1..2

(D) OTHER INFORMATION: /note= "Xaa in position 1 is
pyroglutamic acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Xaa Glu Asp Xaa Lys

1 5

[illegible]

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